

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Gln	Glu	Gln	Ala	Ser	Gln	Gln	Ile	Leu	Ser	Ser
1				5					10	

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Met	Thr	Ile	Asn	Tyr	Gln	Phe	Gly	Asp	Val	Asp	Ala	His	Gly	Ala	Met
1			5					10					15		
Ile	Arg	Ala	Gln	Ala	Gly	Leu	Leu	Glu	Ala	Glu	His	Gln	Ala	Ile	Ile
	20						25					30			
Arg	Asp	Val	Leu	Thr	Ala	Ser	Asp	Phe	Trp	Gly	Gly	Ala	Gly	Ser	Ala
	35					40						45			
Ala	Cys	Gln	Gly	Phe	Ile	Thr	Gln	Leu	Gly	Arg	Asn	Phe	Gln	Val	Ile
	50				55						60				
Tyr	Glu	Gln	Ala	Asn	Ala	His	Gly	Gln	Lys	Val	Gln	Ala	Ala	Gly	Asn
65				70				75						80	
Asn	Met	Ala	Gln	Thr	Asp	Ser	Ala	Val	Gly	Ser	Ser	Trp	Ala		
			85									90			

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Met	Ser	Phe	Val	Thr	Thr	Gln	Pro	Glu	Ala	Leu	Ala	Ala	Ala	Ala	Ala
1			5					10					15		
Asn	Leu	Gln	Gly	Ile	Gly	Thr	Thr	Met	Asn	Ala	Gln	Asn	Ala	Ala	Ala

50

	20		25		30										
Ala	Ala	Pro	Thr	Thr	Gly	Val	Val	Pro	Ala	Ala	Ala	Asp	Glu	Val	Ser
	35				40							45			
Ala	Leu	Thr	Ala	Ala	Gln	Phe	Ala	Ala	His	Ala	Gln	Met	Tyr	Gln	Thr
	50				55							60			
Val	Ser	Ala	Gln	Ala	Ala	Ala	Ile	His	Glu	Met	Phe	Val	Asn	Thr	Leu
	65				70					75			80		
Val	Ala	Ser	Ser	Gly	Ser	Tyr	Ala	Ala	Thr	Glu	Ala	Ala	Asn	Ala	Ala
				85					90				95		
Ala	Ala	Gly													

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Met	Ser	Phe	Val	Thr	Thr	Gln	Pro	Glu	Ala	Leu	Ala	Ala	Ala	Ala	Ala
1				5				10					15		
Asn	Leu	Gln	Gly	Ile	Gly	Thr	Thr	Met	Asn	Ala	Gln	Asn	Ala	Ala	Ala
	20						25						30		
Ala	Ala	Pro	Thr	Thr	Gly	Val	Val	Pro	Ala	Ala	Ala	Asp	Glu	Val	Ser
	35						40					45			
Ala	Leu	Thr	Ala	Ala	Gln	Phe	Ala	Ala	His	Ala	Gln	Met	Tyr	Gln	Thr
	50				55						60				
Val	Ser	Ala	Gln	Ala	Ala	Ala	Ile	His	Glu	Met	Phe	Val	Asn	Thr	Leu
	65				70				75			80			
Val	Ala	Ser	Ser	Gly	Ser	Tyr	Ala	Ala	Thr	Glu	Ala	Ala	Asn	Ala	Ala
				85					90				95		
Ala	Ala	Gly													

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Asp Pro His Ala Met Arg Asp Met Ala Gly Arg Phe Glu Val His
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Arg Asp Met Ala Gly Arg Phe Glu Val His Ala Gln Thr Val Glu
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Arg Phe Glu Val His Ala Gln Thr Val Glu Asp Glu Ala Arg Arg
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Ala Gln Thr Val Glu Asp Glu Ala Arg Arg Met Trp Ala Ser Ala

1 5 10 15

(1) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Asp Glu Ala Arg Arg Met Trp Ala Ser Ala Gln Asn Ile Ser Gly

1 5 10 15

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Met Trp Ala Ser Ala Gln Asn Ile Ser Gly Ala Gly Trp Ser Gly

1 5 10 15

(3) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Gln Asn Ile Ser Gly Ala Gly Trp Ser Gly Met Ala Glu Ala Thr

1 5 10 15

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Ala	Gly	Trp	Ser	Gly	Met	Ala	Gln	Ala	Thr	Ser	Leu	Asp	Thr	Met	Thr
1				5				10						15	

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Met	Ala	Gln	Ala	Thr	Ser	Leu	Asp	Thr	Met	Ala	Gln	Met	Asn	Gln
1				5				10					15	

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Ser	Leu	Asp	Thr	Met	Ala	Gln	Met	Asn	Gln	Ala	Phe	Arg	Asn	Ile
1				5				10					15	

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Ala	Gln	Met	Asn	Gln	Ala	Phe	Arg	Asn	Ile	Val	Asn	Met	Leu	His
1			5					10					15	

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Ala	Phe	Arg	Asn	Ile	Val	Asn	Met	Leu	His	Gly	Val	Arg	Asp	Gly
1			5					10					15	

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Val	Asn	Met	Leu	His	Gly	Val	Arg	Asp	Gly	Leu	Val	Arg	Asp	Ala
1			5					10					15	

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Gly	Val	Arg	Asp	Gly	Leu	Val	Arg	Asp	Ala	Asn	Asn	Tyr	Glu	Gln
1				5					10				15	

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Leu	Val	Arg	Asp	Ala	Asn	Asn	Tyr	Glu	Gln	Gln	Glu	Gln	Ala	Ser
1				5					10				15	

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Asn	Asn	Tyr	Glu	Gln	Gln	Glu	Gln	Ala	Ser	Gln	Gln	Ile	Leu	Ser	Ser
1				5					10				15		

(2) INFORMATION FOR SEQ ID NO:50:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Met	Ala	Ser	Arg	Phe	Met	Thr	Asp	Pro	His	Ala	Met	Arg	Asp	Met	Ala
1				5					10					15	
Gly															

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Met	Thr	Ile	Asn	Tyr	Gln	Phe	Gly	Asp	Val	Asp	Ala	His	Gly	Ala
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Gln	Phe	Gly	Asp	Val	Asp	Ala	His	Gly	Ala	Met	Ile	Arg	Ala	Gln
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Mycobacterium tuberculosis
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Asp Ala His Gly Ala Met Ile Arg Ala Gln Ala Ala Ser Leu Glu
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Mycobacterium tuberculosis
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Met Ile Arg Ala Gln Ala Ala Ser Leu Glu Ala Glu His Gln Ala
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Mycobacterium tuberculosis
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Ala Ala Ser Leu Glu Ala Glu His Gln Ala Val Val Arg Asp Val
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:

58

(A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Ala	Gln	His	Gln	Ala	Ile	Val	Arg	Asp	Val	Leu	Ala	Ala	Gly	Asp
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Ile	Val	Arg	Asp	Val	Leu	Ala	Ala	Gly	Asp	Phe	Trp	Gly	Gly	Ala
1				5				10						15

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Leu	Ala	Ala	Gly	Asp	Phe	Trp	Gly	Gly	Ala	Gly	Ser	Val	Ala	Cys	Gln
1				5				10						15	

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(iii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Phe	Trp	Gly	Gly	Ala	Gly	Ser	Val	Ala	Cys	Gln	Glu	Phe	Ile	Thr
1				5						10				15

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Gly	Ser	Val	Ala	Cys	Gln	Glu	Phe	Ile	Thr	Gln	Leu	Gly	Arg	Asn
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

Gln	Gln	Phe	Ile	Thr	Gln	Leu	Gly	Arg	Asn	Phe	Gln	Val	Ile	Tyr	Glu
1					5				10						15
Gln Ala															

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

60

(B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Arg	Asn	Phe	Glu	Val	Ile	Tyr	Glu	Gln	Ala	Asn	Ala	His	Gly	Gln
1				5				10					15	

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Ile	Tyr	Glu	Glu	Ala	Asn	Ala	His	Gly	Gln	Lys	Val	Gln	Ala	Ala
1				5				10					15	

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Asn	Ala	His	Gly	Gln	Lys	Val	Gln	Ala	Ala	Gly	Asn	Asn	Met	Ala
1				5				10					15	

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids
 (B) TYPE: amino acid

61

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Lys Val Gln Ala Ala Gly Asn Asn Met Ala Gln Thr Asp Ser Ala
5 5 10 15

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Gly Asn Asn Met Ala Gln Thr Asp Ser Ala Val Gly Ser Ser Thr Ala
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

Asp Ala His Gly Ala Met Ile Arg Ala Leu Ala Gly Leu Leu Glu
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

Asp	Ala	His	Gly	Ala	Met	Ile	Arg	Ala	Gln	Ala	Gly	Leu	Leu	Glu
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

Met	Ile	Arg	Ala	Leu	Ala	Gly	Leu	Leu	Glu	Ala	Gln	His	Gln	Ala
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Met	Ile	Arg	Ala	Gln	Ala	Gly	Leu	Leu	Glu	Ala	Gln	His	Gln	Ala
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Mycobacterium tuberculosis*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:
- | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Gly | Leu | Leu | Glu | Ala | Glu | His | Gln | Ala | Ile | Ile | Ser | Asp | Val |
| 1 | | | | 5 | | | | 10 | | | | | | 15 |
- (2) INFORMATION FOR SEQ ID NO:72:
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Mycobacterium tuberculosis*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:
- | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Gly | Leu | Leu | Glu | Ala | Gln | His | Gln | Ala | Ile | Ile | Arg | Asp | Val |
| 1 | | | | 5 | | | | 10 | | | | | | 15 |
- (2) INFORMATION FOR SEQ ID NO:73:
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Mycobacterium tuberculosis*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:
- | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Glu | His | Gln | Ala | Ile | Ile | Ser | Asp | Val | Leu | Thr | Ala | Ser | Asp |
| 1 | | | | 5 | | | | 10 | | | | | | 15 |
- (2) INFORMATION FOR SEQ ID NO:74:
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Ala	Glu	His	Gln	Ala	Ile	Ile	Arg	Asp	Val	Leu	Thr	Ala	Ser	Asp
1			5				10						15	

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Ile	Ile	Ser	Asp	Val	Leu	Thr	Ala	Ser	Asp	Phe	Trp	Gly	Gly	Ala
1			5				10						15	

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Ile	Ile	Arg	Asp	Val	Leu	Thr	Ala	Ser	Asp	Phe	Trp	Gly	Gly	Ala
1			5				10						15	

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(4) ORIGINAL SOURCE:

(A) ORGANISM: *Mycobacterium tuberculosis*

(XX) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

Leu Thr Ala Ser Asp Phe Trp Gly Gly Ala Gly Ser Ala Ala Cys Glu
1 5 10 15

(2) INFORMATION FOR SEO ID NO: 78:

[illegible]

(b) LENGTH: 15 amino acids

(10) TYPE: amino acid

(0) STAMPEDNESS: single

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(0) TOPOLOGY: linear

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EC:1.4.1.14 MOLECULAR WEIGHT: 7890

(4) ORIGINAL SOURCE.

(A) ORGANISM: *Mycobacterium tuberculosis*

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Phe Trp Gly Gly Ala Gly Ser Ala Ala Cys Gln Gly Phe Ile Thr
 1 5 10 15

(2) INFORMATION FOR SFO ID NO: 79:

1.8) SEQUENCE CHARACTERISTICS:

AAI LENGTH: 15 amino acids

AM TYPE: amino acid

(c) STRANDEDNESS: single

{D} TOPOLOGY, linear

{4} MOLECULE TYPE: peptide

(iv) ORIGINAL SOURCE:

(A) ORGANISM: *Mycobacterium tuberculosis*

Call SEQUENCE DESCRIPTION: SEQ ID NO: 75:

Gly Ser Ala Ala Cys Gln Gly Phe Ile Thr Gln Leu Gly Arg Asn
1 5 10 15

(2) INFORMATION FOR SED ID NO: 86:

4. SOURCE CHARACTERISTICS:

181 LENGTH: 1.5 mm 250 053 0530

18) TYPE: amino acid

10) STANDOFFNESS: single

(1) TOPOLOGY: linear

(21) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

Gln	Gly	Phe	Ile	Thr	Gln	Leu	Gly	Arg	Asn	Phe	Gln	Val	Ile	Tyr
1					5				10				15	

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

Val	Thr	Thr	Asn	Phe	Phe	Gly	Val	Asn	Thr	Ile	Pro	Ile	Ala	Leu	Asn
1				5				10					15		
Gln	Ala	Asp	Tyr	Leu	Arg	Met	Trp	Ile							
				20				25							

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Asn	Glu	Ala	Asp	Tyr	Leu	Arg	Met	Trp	Ile	Gln	Ala	Ala	Thr	Val	Met
1				5				10					15		
Ser	His	Tyr	Gln	Ala	Val	Ala	His	Glu							
				20				25							

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 467 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

TSAGCCGCCAA	CGTTACCCCTC	GTTTCGTCAC	ACGGACCGGA	TGGCTGCTC	CCCGGACTGC	50
CGCTAGGGTC	GCGGATCACT	CGGCTAGGC	GCGCTTGGC	CCACCGATG	GCGTTCCTC	100
ACAGTTGGGT	TGCGCCGCCG	CCATCGGCCG	GATACCGCA	TGACCTCAGC	TGGCCAGAAA	150
TGACATGCT	CCCAAGGCG	TGAGCACCCG	AGACAACTA	AGACGGAGAT	CGCATGCCGT	200
TTGTGACTAC	CCAGCCGAA	GCTCTGCGCG	CGCGCCCGG	CAGTTGTCAG	GGAATCGGCT	250
CGCATGTA	CGCCGCAAT	GCGCTCGCG	CGACTCCAC	GACGGGGGTG	GTCCCGCGGC	300
CGCCATGAA	NTTTCGCGC	TGAGGCGCG	TGAGTTGCG	GCCACGCTC	AGATCTATCA	350
GCGCTCAGC	GCCCGGCGC	CGCGGATCA	CGAGATGTC	GTCAACACTC	TACAGATGAG	400
CTCAGGCTC	TATGTTGCTA	CGAGGCGCG	CAACCGCGC	CGCGCGGCT	AGAGGACTCA	450
CTGCGATGGA	TTTGGGGCG	TGCGCGCGG	AGGTCAATC	GGTGGGATG	TATGCGGTC	500
CTGGTGGGC	ACCAATGCTC	GCTGCGGCT	CGGCTTGGAA	CGGTTGGCC	GCGGATGTA	550
GTTCGCGGC	CACCGTTAT	GAGACGATG	TGACTCAGCT	CAGCAGTAG	GCTGCGCTAG	600
GTCCCGGCT	ACCGCGATG	GCGGAGCGA	TGCGCGCTA	TGTGGGCTG	ATGAGTGGC	650
CTGCGCGCA	AGCGGAGCG	GCGGCGCAC	AGCGGAGCG	CGCGCGGCT	GCTTTGAGG	700
CGCGTTTGC	CGGACGCTG	CCTCGCGCT	TGATCGCGG	CAACCGGCT	TGCTTGAATGC	750
AGCTGATCTC	GACGATCTC	TTTGGTCAGA	ACACCTCGG	GATCGCGCC	GCGGAGGCTC	800
AGTACGG						850

(i) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

Met	Ser	Phe	Val	Thr	Thr	Gln	Pro	Glu	Ala	Leu	Ala	Ala	Ala	Ala
1			5					10					15	

(i) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

Thr	Gln	Pro	Glu	Ala	Leu	Ala	Ala	Ala	Ala	Asn	Leu	Gln	Gly	
1			5					10				15		

(i) INFORMATION FOR SEQ ID NO:86:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

Leu	Ala	Ala	Ala	Ala	Ala	Asn	Leu	Gln	Gly	Ile	Gly	Thr	Thr	Met
1					5				10					15

(2) INFORMATION FOR SEQ ID NO:87:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

Ala	Asn	Leu	Gln	Gly	Ile	Gly	Thr	Thr	Met	Asn	Ala	Gln	Asn	Ala
1					5				10					15

(2) INFORMATION FOR SEQ ID NO:88:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

Ile	Gly	Thr	Thr	Met	Asn	Ala	Gln	Asn	Ala	Ala	Ala	Ala	Ala	Pro
1					5				10					15

(2) INFORMATION FOR SEQ ID NO:89:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

Asn	Ala	Gln	Asn	Ala	Ala	Ala	Ala	Ala	Pro	Thr	Thr	Gly	Val	Val
1			5						10				15	

(2) INFORMATION FOR SEQ ID NO:90:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(11) MOLECULE TYPE: peptide

(X1) SEQUENCE DESCRIPTION: SEQ ID NO:90:

Ala	Ala	Ala	Ala	Pro	Thr	Thr	Gly	Val	Val	Pro	Ala	Ala	Ala	Asp
1				5				10					15	

(2) INFORMATION FOR SEQ ID NO:91:

(1) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(11) MOLECULE TYPE: peptide

(X1) SEQUENCE DESCRIPTION: SEQ ID NO:91:

Thr	Thr	Gly	Val	Val	Pro	Ala	Ala	Ala	Asp	Glu	Val	Ser	Ala	Leu
1				5				10					15	

(2) INFORMATION FOR SEQ ID NO:92:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(11) MOLECULE TYPE: peptide

(X1) SEQUENCE DESCRIPTION: SEQ ID NO:92:

Pro	Ala	Ala	Ala	Asp	Glu	Val	Ser	Ala	Leu	Thr	Ala	Ala	Glu	Phe
1				5				10					15	

(2) INFORMATION FOR SEQ ID NO:93:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

Glu	Val	Ser	Ala	Leu	Thr	Ala	Ala	Gln	Pro	Ala	Ala	His	Ala	Gln
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

Thr	Ala	Ala	Gln	Pro	Ala	Ala	His	Ala	Gln	Met	Tyr	Gln	Thr	Val
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

Ala	Ala	His	Ala	Gln	Met	Tyr	Gln	Thr	Val	Ser	Ala	Gln	Ala	Ala
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

Met	Tyr	Gln	Thr	Val	Ser	Ala	Gln	Ala	Ala	Ala	Ile	His	Gln	Met	Pro
1				5							10				15

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

Ser	Ala	Gln	Ala	Ala	Ala	Ile	His	Glu	Met	Phe	Val	Asn	Thr	Leu
1				5					10					15

(i) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

Ala	Ile	His	Gln	Met	Phe	Val	Asn	Thr	Leu	Val	Ala	Ser	Ser	Gly
1				5					10					15

(i) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

Phe	Val	Asn	Thr	Leu	Val	Ala	Ser	Ser	Gly	Ser	Tyr	Ala	Ala	Thr
1				5					10					15

(i) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

Val Ala Ser Ser Gly Ser Tyr Ala Ala Thr Glu Ala Ala Asn Ala
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

Ser Tyr Ala Ala Thr Glu Ala Ala Asn Ala Ala Ala Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1784 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

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ATTGGTTCCT GCGGCACTA AATCCCGGGG ACATCGTCGC CGGKCACTAC GAGGTCAAAG      60
GCTGCATCCG GCGCGGCGGA CTGGGCTGGA TCTACCTCCG TCTCGACCGG AATGTCAACG      120
GCGGTCGGGT GGTGCTCAAG GGCCTGGTGC ATTCCGGTGA TGCCGAAGCG CAGGCAATGG      180
CGATGCGCGA AGCGCAGTTC CTGGCGGAGG TGGTGACGCG GTCCATCTTG CAGATCTTCA      240
ACTTTGTGGA GCACACCGAC AGGCGCGGGG ATCCGGTCTGG CTACATCTTG ATGAATATG      300
TCGGCGGCGA ATCGCTTAAA CGCGGCAAGG GTCAAAACT GCGCTCCCG GAGGCCATCG      360
CTTACCTCTCT GAGATCTGCG CCGCGGCTGA GTTACCTGCA TTCCATCGCG TTGCTCTACA      420
ACGACTCTGA GCGGAAAAAC ATCATGCTGA CCGAGGAACA GGTCAAGCTG ATCCACCTTG      480
GCGCGGTATC GCGGATCAAC TGTTCGGGCT ACCCTACCG GACCCGAGG TCCAGGCGC      540
CTGAGATGCT GCGGCGCGGT CCGACGGTGG CCACGCGCAT CTACACCTTG GAGCGCACG      600
TCGCGCGGCT CAGCTGCGAC CTGCGCACCC GCATGCGCG TTATGTGAT GGCCTACCG      660
AAGACGACCC GTTGTGAAA ACCTACGACT GTTACGCGCG GTTCTGCGG AGGGGATCG      720
ACCTCGATCC GCGGCAACGG TTCAACACCG CGGAGAGAT GTCCGCGCAA TTGACGGGG      780
TGTTGCGCGG GTTGGTCCGC CAGACACCGG GGTCCGCGG CCAAGCTATC AACGATCTTC      840
AGTCCGAGTG GTTCGACTT TGAAGTGGAC TGTGCTGCG GACAGCGCAC GTGTATGTGG      900
ACGGGACAGT GCACGCGGAG AAGCTGACCG CCAACGAGAT CGTGACCGAG CTGTGCGTGC      960
CGGTGATCGG TCGGACCGAC GTGCGCAGTT CGGTCTGCG GGCACCGGTC CTCTCCCAAG      1020
CGGTGCACAG CCTAGACTCG GTGCGCGCGG CCGGCGCACG TGTGCTGAG GCGGATCGGT      1080
TCAATTTGCG GATTCAGTGG ACGTCCCGCT AATGGAAGTC CCGCGCGTGC TGATCTTCGG      1140
CGATGTGGCC AAGCGCACCC GAAACCTCGA CATCTGCGC GACCGCGTGG GCTGGGCAAG      1200
CGGATTCGTC TGCTACCGCG CGTTGCGCGA GTTGTCTACT GGTGACTATG ACTTGGCGAC      1260
CAAACTTTTC ACCGAGGTGC TGAATACCTT TCCCGGCGAG CTGGCGGCGA AGCTGGCGCT      1320
GCGCGCTACC GCGCAATTCG CGGCAACAGC GACGGAACAC AAGTCTATG AGACGCTGTA      1380
GACGACACAC GACCGAGTGG TCTGCGCGCG TTTCGAGCTG GTCAGAGCCC GTTCGCGCGA      1440
AGGTGATCGG GTCGGCGCGG TCGGCAAGCT CAGCAGGATA CGGCGACCTT CTGGGCAATT      1500

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CACCACGGCA	CGGGTACTA	GCGGCTGAC	TCGTGTGTC	GGCGGTCAA	CGAGTGAAT	1560
CACGACGAA	CAGATCCGC	ACGTCGCGC	AAGAGTGGG	CGCGTGCCT	CGACCGAAC	1620
ACGGTCTCT	CAGATCCGC	CGCTGTCTT	GGGTGGGCG	CTGGATGGC	TGAGGACAA	1680
CAAGCGGAG	ACGACGACA	TCCTGGGTT	CGCGTTGAG	AGTCAGGAG	TGCGGTGGG	1740
TGTCAGGCG	TCAGTCGCA	GCTTGGGCG	GATGCTGCT	ACTC		1784

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 766 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

ACAARACACT	CGGTGGCGCC	CGGTGCGCC	TGATGTCGG	TGATCAGCT	CGTGCCAAAY	50
TGGCGCAAG	GTGCGCGCT	CCCAAGAGT	TCTTGGCGC	GTGCGGCGC	KAACGCGCT	120
ATCTGCTTG	GGTGGCTTC	CGCAAAAGC	GCGACTTAA	ACCTATTTA	ACCGGCGAG	180
AAGTTTCTA	CTTTGACCC	GGGAAACCA	CGGGGCGCC	NANAACTCG	TCTTGANTC	240
CGANCGCTT	CGGTGTTTC	CGGCTGCTT	GAGCGGCGC	GATATCTTC	AGCGGCTTT	300
GGCGAGGCG	TGGTTCAGC	TGGCTTGGG	TGGGACGAC	GAGGCGATC	CGGCTCGGA	360
GTCCGACCA	GTACTCAAT	CTTGGGAGC	CACCGGCGC	CAGACCAAC	TGTTGACGC	420
CGATCTCCG	CGGCGCGCG	CGGTGGGAT	ACGGATTGT	CGAAACCAAT	CGGAAGGAT	480
TCATCAGCA	CGGTGCGGA	AAACGATCG	CGCAATGGG	GAATNACCG	AGCGAGCGG	540
ATTNACGTT	NAACAGTTG	GGTATGTTT	TTTATCTTC	AKTACCGAT	ACGAGCGCG	600
CGCGGAATC	TGAGCGGCG	ACGAGTGGC	GAAGTATTC	CACGATTTT	GTCTCGGCG	660
CGAGATGCT	CGCGGCGCA	AGCTTTCGG	ATCGGAGAT	GAAGTATTC	AGCTTGGTG	720
ACTGTGTTG	CAGGTGTTT	CAGTGGGCG	TGGGAGGCT	GCGGAT		766

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1331 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

CGGACAGGA	ATGTCGCTT	TGCTGATA	GCGACTTGC	TGCTGCTGC	CTGGCAGGG	50
GTGCGGAGG	TGGCGTGTG	CAGGCTATG	GCGGCGGCA	GAGCGGAGT	CTTGGCGAG	120
CTGCTGTAC	GAGAGCGGA	CTGAGGAGG	TGTCGCGCT	GAGCGGAGT	CAGTGTGGG	180
CAGACGCGA	GATCTATCG	CGCTGATCG	CUCAGGCGC	GGGATTCAC	GAGATGTTG	240
TCAGACGCT	ACAGATNAC	TCAGGCTGT	ATGCTGCTAC	CGAGCGGCG	AAAGCGGCG	300
CGGCGGCTA	GAGAGCTAC	TGCGATGAT	TTTGGGCGT	TGCGCGGGA	GCTCATTCG	360
GTGCGGCTT	ATGCGGCTT	TGCTGCGCA	CGAATGCTG	CTGCGGCGT	CGCTGGAAC	420
GGTGTGCGG	CGAGCTGAG	TTGCGGCGC	ACCGGTTAT	AGAGGTTAT	CAGCTGAGT	480
AGGATGAGG	GTTGCTTAG	TGCGGCTCA	GCGGCTATG	CGAGGAGAT	TGCGGCTAT	540
TGCGGCTGA	TGAGTGGCG	TGCGGCGCA	CGGAGGAGG	CGGAGGAGG	CGGAGGAGG	600
GCGCGGCGG	CTTTGAGGC	GCGGTTGCG	GCGAGGAGG	CTCGGCGGT	GATGCGGCG	660

AACCGGGCTT	CGTTGATGCA	GCTGATCTCG	ACGGAATGCT	TTGGTCAGAA	CACCTCGGCG	720
ATCGCGGCTG	CGGAGCTCA	GTACCGCGAG	ATGCGGGGCG	AAGACTCCGC	GCGGATGTAT	760
GCGTACGGCG	GCACTTCGGC	GAGCGGCTCG	CGCGTCACGC	CGTTAGACAC	GCGCGCGCAG	840
ATTGCCAAGG	CGAGCGCTCA	GGGTACGGAG	GCGCGCGCGG	TGGCCACCGC	GCGCGGTACC	900
GCGCAATCGA	CGCTGACGGA	GATGATCACT	GCGCTACCGA	ACGCGCTGCA	AAAGCTCAGC	960
TGCATCTGTT	TGGGCTGCTG	TACAGGTCGG	CTGCTGTGCG	TGTCGACGAT	CTGTGTGCGC	1020
ACCGCGGATT	TGCGGACCTG	AATTTGCGCA	CTGCTGACCG	ACGTGACAGC	CTAGCGGAGC	1080
TTTGTATATA	ACACCGAGGG	CTTGCGGTCG	TTGACGATCG	GCATGCGCAA	CAACTTCAAT	1140
CAGTCTGCTA	AGACCTTGGG	ATTGATCGGC	TAGGCGGCTG	CGACTGCAAT	GCGCGGTGCT	1200
GCGGATTCGG	CGGAGGCTTT	GCGCTGTGCG	G			1231

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2041 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

CGGCACGAGC	TGTTGCGGAT	CAATGCGGCT	GAGCGCTTGT	ACGACCTTCT	GGGCGTTGGA	60
ATACCCAGCC	AAGGGGGTAT	CTTTTACTTC	TCACTAGAGT	ACTTCGAAAA	AGCGCTGGAG	120
GAGCTGGGAG	CAGCGTTTCC	GGGTGATGCG	TGGTTAGGTT	GCGCGCGCGA	CAAAATACCGC	180
GCGAAAAGCC	GTAACACAGT	GAATTTTTTC	CAGGAGCTGG	CAGAGCTTGA	TGTCAGCTCC	240
ATCAGCTTGA	TCTACGACCA	GCGCAACGCG	GTTCAGACGA	CGCGCGACAT	CTTGAGAGGC	300
GCGAAGAAAG	GTCTGAGTTC	CGTGGCGCGG	GTGCTGTGCG	ACCTGACCTA	CATCCCGCTC	360
TGCGGCGGCG	CGCTATCGCG	GCGCTTCGAG	GCGCGCTTTC	GCGCGGCGCG	GATGCGCGTA	420
GTCGCGCGCG	CGCTTGCTTA	CTTGCTGCTG	AAAACGCTGA	TCAACCGGAC	TCAACTCTTC	480
AAATTGCTTG	CTAAATTGGC	GGAGTTGCTC	GCGGCGCGCA	TTCGCGACAT	CATTTCGAGT	540
GTGCGGAGCA	TCTATCAAGG	CATGCTCGGA	GAAGTGTGCG	AGTTTATCAC	AAACCGCGCTC	600
AACGCGCTGA	AAGAGCTTTG	GGACAGCTTC	ACGCGGTTGG	TGACCGGACT	GTTCCTCTCGA	660
GAGTGTGCGA	ACCTGGAATC	CTTCTTTGCG	GCGCTCGCGG	GCTTGACCGG	GCGGACGAGC	720
GCGTGTGCGC	AAGTACTGCT	CTTGTTCGCT	GCGCGCGCTG	TGTCGCGATC	GTGCGGCTTG	780
GCTCAGCGCG	ATAGCTTGCG	GAGCTCAAGC	AGCTTGGCGG	CGCTGGGCTG	CATTGAGGCG	840
GCGTCTGCTT	TGGGCGCTT	GCGGAGCTTG	GCTCAGGTCG	ATCGCGCTTC	AGCTGAGGAG	900
GCGCTACGCG	CGCGAGCTGA	TGGCGCGGTC	GCGCGCGCTG	CGGAGCGAGT	GCGCGGCGAG	960
TGCGAGCTGG	TCTCGCGCGA	GCGTTCGCAA	GCTATGCGCG	GACCGCTAGG	CATCGCGCGG	1020
ATGCAAGGCT	CTTCGCGGCG	GTGAAAAGCG	ACGACGACGA	AGAGTACTC	GGAGCGCGCG	1080
GTGCGCGGCA	GTGAGAGAGC	CGAGCGCGCG	CGAGTCGAAG	GTGAGCGCGG	GCGTGGCGAA	1140
AAGGTGCTGG	TACGAAAGCT	CGTCTAACGG	CATGCGGAGC	CAAACTCAAT	GCTAGCGAGC	1200
GCTTACAGAC	GCGCAATGCT	AACCGGAAGG	GACACAGTCA	ATGCGCGAAA	ACTTTCAGCT	1260
CGAGCTCGAG	CGTCTGCTGG	TACTGCGCTC	GCACTATGAG	AACGCGCGCG	TGCGATGCTG	1320
CTGCGGCTGC	GAAATCTGCT	CTGCGCTAGG	GCAATCTGCG	GCAATCTGCT	GCGTCTGCTA	1380
CTGCTCAGAG	TTCAACGACA	CGTAAATGCT	GTACTTGAAT	GCGGCAAGT	CGCTGCGCTC	1440
CTGCTTCTAG	ACGCGCGGTT	TGCTTCTGCG	CRAAGTCTTT	GCAATTCGCG	GCAAGATATA	1500
TACCGAGGCG	GACGAAATGCT	GCGCGAAGCG	TATCGAGCGG	TGCTTTCAGT	GCGAGGCTTT	1560
CTGCGCGGCA	GTGCGAGCCA	CAAGCTAGCG	CAGGTCGCTT	CGCTCTGAGG	CTGCTATGCG	1620
ACCGCGCAGC	ACCGAGCAGC	GTGCGGCGCG	GATGCGGCGG	GACAGTAGAG	GCGCGGAGTG	1680
CGCGGCTGCG	GTGCGGCGCA	CAAAACCGCG	CAGTTCGCGC	TGCGCGACGA	GCGTGTGCTG	1740
GGAATCCAGC	GCGCGAAGCG	CGGTAATGCG	TGCGAGCGCG	AGCAGGAGCG	AGAGTCTGAT	1800
TTTTCGCGAT	CGGTCGCGCG	CAGCGATGAG	GTGCGGCGCG	CGCGGCGCGG	GTGCTTCTGAG	1860
ATCGGCGGCG	GCGTACGCTA	CAGTGGGCGA	GCTTACTGCA	GCGCTCTGCT	GCGGAGCGCG	1920

TGCTTGTCGA	TGAGTACTAG	CGAGCATGCC	AGCAGCCAGG	GCATCCGACC	GGTGTGAGGA	1980
ATTGTGTCGG	CGCCGTGCTG	GGGAGCTGCT	CGAGCTCTCT	CATGCCATCC	ACCTGTGCTC	2040
9						2041

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1202 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

GAGCTCACC	CTATCAACCA	ATACTTTCTG	CGCTCCAGAG	TGCAGGACAA	CTGGGCTTTT	60
ACCGAGTGG	CGGCCCCAGC	CCGCGCGGAG	TGTTTCGACG	AAATCGGGCA	CGCCGAGGGA	120
ATCAGCATC	GCATCTTTT	GCTGGATGGT	TTGCGGAAT	ACCAAGCGAT	CGTTTGGTTC	180
CGTATCGCC	AGAGCTCCG	CGAGCAATTT	GAGCGCGATC	TGGCGATCGA	ATACGAGGTG	240
TTGATCTCT	TGAGCCGAG	AATCTCTATG	TGCGCGGAGA	AGCAGGACAC	CACCAAGGCC	300
GTACTGCTGG	AGAAATCTGT	TGCGGACGAG	GAGAGACACA	TGACTACTT	GGAAACGCGG	360
CTGAGCTGA	TGACAAAGCT	AGGAGAGGAG	CTTTACTCGG	CGCATTCGCT	CTCTCGCCCA	420
CGGACCTGAT	CGCCGCTTGA	GGATTCTCGG	ATACCATCTC	GGGCGCCGCT	GACAGCTCTT	480
AGCATGAGCT	CGAAGACGGA	TGGAGGGGCG	GATATGGGCG	CGCCCGAGC	ACCGACCACT	540
CGCCGAGCAG	CAATTCAGAG	CGGTGCCCCG	CTGCTCAGTC	CGGTGCGAGC	CAACATTATT	600
TTCAAGGCGG	TTGGGTCGCG	GGTGCTGATC	GTTCGCGACC	GCCAAAGCAT	CGTGGGAGCC	660
CGATTGCCGA	CGATCTCTCG	CGAGCTGAGG	AGCAGCTTGG	ACCACTCTCT	GGCGGTCACC	720
AGCTATCTGC	TGGGGGGAAC	ACTSKYGEFF	KYGAKKKSKS	ESRKNKCTC	GGTGATCTGC	780
TGGGCGCCAA	CAGGTTGCTG	CTAGGCTCCG	TGTTGCTCTT	CGTCGTTGGC	TCCTGCTCTT	840
GGGGGTTATC	CGAGAGCATG	ACCATGCTGG	CGATCTCTCG	CGCACTGCAG	GGCGTGGGTG	900
CGGGTGCGAT	TTCTGTCACG	GCTTAGGCGG	TGGCGCGTGA	GGTGATCCCA	CTGCGGAGCC	960
CTGGGCGCTA	CTAGGGGCTC	TTAGTGTGCG	TTTCTCGTGT	CAACACGGTC	ACCGGTCCGC	1020
TGCTGGGGGA	CTGGCTCACG	GACTATCTGA	GCTGCGGTG	GGCGTCCGCA	CTACCAAGGC	1080
CATCACCGAC	CGGATCGCGG	TGATTCGCGG	GAAACCTCC	CTCGCGGGCT	TGCGGGCAGG	1140
TGCTTGGGG	AACTGTGCTC	CACAGCGCGC	GAAGGCTCG	AAATGGGATG	GGCAGCCAC	1200
AC						1202

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 456 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

GGCGGCGCA	GTTGCGCAG	AGTTGGGCG	GGGGAGCCGG	TTGGGAGGAC	AGGAAATCGG	60
CCYGGGCAAG	CGGCGGAG	CGCGGACCTT	GATCTATTGA	GATCGGCGCG	ACCGCCCGCG	120
ACCAAGGCGA	TTGCGCGGTT	GAGGAGATCG	GAATNTTGGC	CACTGATGAC	CGCTCTCTCG	180
AAAGCTTCCC	GGATTCTCGA	GGGATCCGCC	CGCGAACCGC	GGTCTCTACG	ACCGCGGAGG	240
ACCGCTGAGG	ACAGGCTCCG	ATAGCTGAGT	GAGGCGGGGT	NACCGGCTTC	CGTCTGCGCG	300

NGANATCGGC	CGGAGACAA	AAGATCGCTC	GCGGCTCGGC	CTCGGCGACG	ACAGCCACCT	360
TCACCCGCGC	GTATTCGCTG	GCGCGCTGCG	CATACCAGGC	GCTGTCGAAG	TGCGGTCTGC	420
GGTAGTCACG	CACGACAAAG	GTGATTTGGT	CGATCGCTTC	GACGCGCGCG	GTGACGCTGC	480
GCGCATCAAT	GTGCAC					495

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 849 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

TGGATTCCGA	TAGCGGTTTC	GCCCCCTCGA	CGGGGACCCA	CGGGCGCGAG	GLCTCCGAAC	60
GGGGGCGCGG	GACGCTGGGA	TTCCGCGGGA	CGGCAACCAA	AGAACGCGCG	GTCCGCTCGG	120
TGGGGCTGAG	GCGACTGGCC	GCTGATGAGT	TGGCAACCGG	CGCCCGGATG	CGGATGGTGC	180
CGGGGACCTG	GTACGCGGCG	AGCACTGAGC	CGGAGCGCGC	GTACGGATCG	GGCGAGGCGG	240
GAGCGAGCGG	GTACCGCGAC	GACAGCAAGT	AACCGAATTC	CGAATCACCT	GGACCGTAC	300
GCGTCCGAAG	GAGAGATGTT	ATGAGCTTTT	TGATGCTCA	TATCCGACAG	TGTGTGCGCT	360
GCGAGTGGCG	GTTCGCGCGG	AGGGCGCGGC	TGATGCGGCA	CACGATCGGT	CAGCGCGAGC	420
AGGGCGCGAT	GTGCGCTTCA	CGTTTTCACC	AGGGGCGAGC	GTCCGCGCGG	TTTCAGGCGG	480
CCCATGCGCG	GTTCGTGGCG	GCGGCGCGCA	AAGTCAACAC	CTTGTGCGGT	GTCGCGGAGG	540
CGAATTCGGG	TGAGGCGCGC	GCTACTTATG	TGGGCGCGCA	TGCTGCGGCG	GCGTGGACCT	600
ATACCGGHTT	GTGATCGGAG	CTTCTGACCT	GAGAGGACTT	GTGATGTTCG	AAATCATGTA	660
GCACTACGCG	GCGATTTTGG	GTGCGCGCGG	GGATATGAGT	GGATATGCGG	GCACTCTGCA	720
GAGCTTGGGT	GCGGAGATCG	CGTGGAGCA	GCGCGGTTTG	CGAGAGTGCT	GCGCGGCGGA	780
TACCGGGATC	ACGTATTCAG	CGTGGCGGCG	ACATGTGTAA	CGAGCGCGAG	GAGGATTTCG	840
TGCGGCGCTT						849

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

Met	Ser	Leu	Leu	Asp	Ala	Ris	Ile	Pro	Gln	Leu	Val	Ala	Ser	Gln	Ser
1				5				10					15		
Ala	Phe	Ala	Ala	Lys	Ala	Gly	Leu	Met	Arg	His	Thr	Ile	Gly	Gln	Ala
				20				25					30		
Gln	Gln	Ala	Ala	Met	Ser	Ala	Gln	Ala	Phe	Ris	Gln	Gly	Gln	Ser	Ser
				35				40					45		
Ala	Ala	Phe	Gln	Ala	Ala	His	Ala	Arg	Phe	Val	Ala	Ala	Ala	Ala	Lys
				50				55					60		
Val	Asn	Thr	Leu	Leu	Asp	Val	Ala	Gln	Ala	Asn	Leu	Gly	Glu	Ala	Ala
65						70				75				80	

Gly Thr Tyr Val Ala Ala Asp Ala Ala Ala Ala Ser Thr Tyr Thr Gly
85 90 95
Phe

[2] INFORMATION FOR SEQ ID NO:110:

1.1 SEQUENCE CHARACTERISTICS

- (A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

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(xii) SEQUENCE DESCRIPTION: SEQ ID NO:110.

Mar	Ser	Leu	Leu	Asp	Ala	His	Ile	Pro	Gln	Leu	Val	Ala	Ser	Gln
3				5					12					15

(2) INFORMATION FOR SEC ID NO: 215:

1.1 SEQUENCE CHARACTERISTICS

- (A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(11) MOLECULE TYPE: sesquide

(x1) SEQUENCE DESCRIPTION: SFO ID NO. 111.

Ala His Ile Pro Gln Leu Val Ala Ser Gln Ser Ala Phe Ala Ala
1 5 10 15 20

(2) INFORMATION FOR WHO IS NOT:

4.1 SEQUENCE CHARACTERISTICS -

- (A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(11) MOLECULE TYPE: peptide

(61) SEQUENCE DESCRIPTION: SWO ID NO: 112.

Leu Val Ala Ser Gln Ser Ala Phe Ala Ala Lys Ala Gly Leu Met
3 8 13 18

(2) INFORMATION FOR SHO ID NO:113:

(4) SEQUENCE CHARACTERISTICS.

- (a) LENGTH: 15 amino acids
(b) TYPE: amino acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

Ser	Ala	Phe	Ala	Ala	Lys	Ala	Gly	Leu	Met	Arg	His	Thr	Ile	Gly
1				5				10					15	

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

Lys	Ala	Gly	Leu	Met	Arg	His	Thr	Ile	Gly	Gln	Ala	Gln	Gln	Ala
1				5				10					15	

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

Arg	His	Thr	Ile	Gly	Gln	Ala	Gln	Gln	Ala	Met	Ser	Ala	Gln	
1				5				10					15	

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

Gln	Ala	Gln	Gln	Ala	Ala	Met	Ser	Ala	Gln	Ala	Phe	His	Gln	Gly
1				5				10					15	

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

Ala	Met	Ser	Ala	Gln	Ala	Phe	His	Gln	Gly	Glu	Ser	Ser	Ala	Ala
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

Ala	Phe	His	Gln	Gly	Glu	Ser	Ser	Ala	Ala	Phe	Gln	Ala	Ala	His
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

Glu	Ser	Ser	Ala	Ala	Phe	Gln	Ala	Ala	His	Ala	Arg	Phe	Val	Ala
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

Phe Gln Ala Ala His Ala Arg Phe Val Ala Ala Ala Lys Val
1 5 10 15

(1) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

Ala Arg Phe Val Ala Ala Ala Ala Lys Val Asn Thr Leu Leu Asp
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

Ala Ala Ala Lys Val Asn Thr Leu Leu Asp Val Ala Gln Ala Asn
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

Asn Thr Leu Leu Asp Val Ala Gln Ala Asn Leu Gly Glu Ala Ala
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

Val	Ala	Gln	Ala	Asn	Leu	Gly	Glu	Ala	Ala	Gly	Thr	Tyr	Val	Ala	Ala
1				5					10					15	
Asp	Ala														

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1752 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

CGGCAAGAGA	ATGTGGCTTG	TGCTTGGATA	GGCACTTGGG	TGTGGTGGG	CTGCGAGCG	60
GTGAGCCAGG	TGCGCTGTG	CAGGCCATCG	GGCCGGGCGA	GGAGCGGAT	GTGCGGCGA	120
CGCGGTGTAC	GAGAAACGGA	CTGCGCAAG	TGTGGGCGCT	GACGGCGGCT	CAGTTCGCG	180
CACAGCCCTA	GATCTAAGG	GCTGTAGCG	CXLAGGCCGT	GGGATTTTAC	GGATGTTTC	240
TCAACACTCT	ACAGATTAAT	TGAGGTCCT	ATGCTTCTAC	CGAGGCGGCC	AACGGGCGG	300
CGCGCGGCTA	GAGGAGTCAC	TGGATGGAT	TTTGGGCGGT	TGCGCGCGGA	GGTCAATTGG	360
GTGCGGATGT	ATGCGCGTCC	TGACTCGGCA	CCATGTGTCG	CTGCGGCGTC	GGCTTGGAA	420
GGTTTGGCG	CGGAGCTGAG	TTGCGCGGCT	ACCGTTTATG	AGACGATGAT	CACTCAGCTC	480
AGCAGTGAGG	GATGCTTAGG	TGCGGGTCA	GGCGGATAG	CGGAGCGGCT	TGCGGCTAT	540
GTGGCTGGGA	TGAGTGGCG	TGCGCGCGAA	GGCGAGCAGG	CGGCGACACA	GGCCAGGGCC	600
GGCGCGCGCG	CTTTTGAGGG	GGCTTTTGGC	GGGACGGTGC	CTGCGCGCTT	GATGCGCGCC	660
AACCGGGCTT	CGTTGATGCA	GCTGATCTCG	ACGAGCTGCT	TGGTCAGAA	CACCTCGCG	720
ATCGCGCGCG	CGGAGCTCA	GTACGCGGAG	ATTTGGGCCC	AGAGCTGCG	GGGATGTAT	780
GGCTACCGCG	CGAGTTCTGG	GAGGCTCTCG	GGGCTCAGGC	CGTTTACGAC	CGCCCGCGAG	840
ATTGCGAACC	CGAGCGGCTCA	GCGTACGCG	CGCGCGGCGG	TGGCCACGCG	CGCGGCTACC	900
GGCGGATCGA	CGGTACGCGA	GATGATCAGC	GGGCTACCGA	ACCGGCTGCA	AAGCTTCAGC	960
TGCTATGTGT	TGCACTGTTC	TACGCTTGG	CTGTGCTGGC	TGTGGCAGAT	CTTGTTCGGC	1020
ACCGCTCAAT	TGCGGCTGTC	AATTTGCGCA	CTGCTGACCG	AGCTGCGCGG	GTACGCGGAG	1080
TTTNTTATTA	ACACCGAGGG	CGTTCGCTAC	TTTACGATCG	CGATGGGCGA	CAACTCTATT	1140
CAGTGGGCGA	AGACCGTGGG	ATTGATCGCG	TAGGCGGCGA	CGGCTGCGCT	CGCGGCTGCT	1200
GGGATATGAG	CGAAGGCTTT	GCTCTGACTG	GGCGGATGCG	TGGGTGCGCG	GGCGGCTGCG	1260
GGGCTGCTGG	GCAATTCGCG	TTCGCTTGGC	AAGCTGTGCG	TGCGGCTGCT	GTGAGTTGGA	1320
CGTTGCGCG	GCTCTGTTAC	TGCGGCGGCT	GCTCGGCTAC	CGTGTAGTAC	GCTGATGTC	1380
CGCCCGGAGG	CGCGCGCGCG	AAGCTTTTTC	GGCGGCTGCG	CGCTTACGTC	TGCGGCGGCG	1440
CGCGCGCGCG	GTGACGCTTA	CGGATTCGCT	CGGACGCTCA	TGCGCGCGCG	ACCTTTGTCG	1500
GGGATATGCG	CTGCGCGCAC	GTATTACGCT	CGCGGCTTCA	GCTGCTGTCG	CGCGGCTGCG	1560
GTGCAATGCT	GTGCGCGCGG	AAATCTCGCT	GGGTTATTTC	CGGTGGGATT	TTTCTCGGAA	1620
CGCGGCTTCA	GCAGCGGAT	TGCTTACGCT	CGCGGCTTCA	TGCTTGGGAA	TTTCTCGGCTA	1680
ATGAGCTTCC	GGCGGAAATC	GCTTGGGTTT	GAAAGCTTCA	GAAAGCGCGG	CTTCTCGGCG	1740
TTGCGCAAC	GG					1752

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

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Met Asp Phe Gly Ala Leu Pro Pro Glu Val Asn Ser Val Arg Met Tyr
 1          5          10          15
Ala Gly Pro Gly Ser Ala Pro Met Val Ala Ala Ser Ala Trp Asn
 20          25          30
Gly Leu Ala Ala Glu Leu Ser Ser Glu Ala Ala Thr Gly Tyr Glu Thr Val
 35          40          45
Ile Thr Gln Leu Ser Ser Glu Gly Trp Leu Gly Pro Ala Ser Ala Ala
 50          55          60
Met Ala Glu Ala Val Ala Ser Tyr Val Ala Trp Met Ser Ala Ala Ala
 65          70          75          80
Ala Gln Ala Glu Gln Ala Ala Thr Gln Ala Arg Ala Ala Ala Ala Ala
 85          90          95
Phe Glu Ala Ala Phe Ala Ala Thr Val Pro Pro Leu Ile Ala Ala
100          105          110
Asn Arg Ala Ser Leu Met Gln Leu Ile Ser Thr Asn Val Phe Gly Gln
115          120          125
Asn Thr Ser Ala Ile Ala Ala Ala Glu Ala Gln Tyr Gly Gln Met Trp
130          135          140
Ala Gln Asp Ser Ala Ala Met Tyr Ala Tyr Ala Gly Ser Ser Ala Ser
145          150          155
Ala Ser Ala Val Thr Pro Phe Ser Thr Pro Pro Gln Ile Ala Asn Pro
160          165          170          175
Thr Ala Gln Gly Thr Gln Ala Ala Ala Val Ala Thr Ala Ala Gly Thr
180          185          190
Ala Gln Ser Thr Leu Thr Glu Met Ile Thr Gly Leu Pro Asn Ala Leu
195          200          205
Gln Ser Leu Thr Ser Xaa Leu Leu Gln Ser Ser Asn Gly Pro Leu Ser
210          215          220
Trp Leu Trp Gln Ile Leu Phe Gly Thr Pro Asn Phe Pro Thr Ser Ile
225          230          235
Ser Ala Leu Leu Thr Asp Leu Gln Pro Tyr Ala Ser Xaa Xaa Tyr Asn
240          245          250          255
Thr Glu Gly Leu Pro Tyr Phe Ser Ile Gly Met Gly Asn Asn Phe Ile
260          265          270
Gln Ser Ala Lys Thr Leu Gly Leu Ile Gly Ser Ala Ala Pro Ala Ala
275          280          285
Val Ala Ala Ala Gly Asp Ala Ala Lys Gly Leu Pro Gly Leu Gly Gly
290          295          300
Met Leu Gly Gly Gly Pro Val Ala Ala Gly Leu Gly Asn Ala Ala Ser
305          310          315          320
Val Gly Lys Leu Ser Val Pro Pro Val Trp Xaa Gly Pro Leu Pro Gly
325          330          335
Ser Val Thr Pro Gly Ala Ala Pro Leu Pro Val Ser Thr Val Ser Ala

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340				345				350							
Ala	Pro	Glu	Ala	Ala	Pro	Gly	Ser	Leu	Leu	Gly	Gly	Leu	Pro	Leu	Asp
355				360				365							
Gly	Ala	Gly	Gly	Ala	Gly	Ala	Gly	Pro	Arg	Tyr	Gly	Phe	Asp	Asp	Pro
370				375				380							
Val	Met	Ala	Arg	Pro	Pro	Phe	Asp	Gly	Ile	Val	Ala	Ala	Ala	Thr	Tyr
385				390				395				400			

123 INFORMATION FOR SIDS TO SDG 12.7:

1.2. SOURCE CHARACTERISTICS:

(A) LENGTH: 474 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(11) MOLECULE TYPE: GINA

(a) SEQUENCE DESCRIPTION: SEQ ID NO. 127

ACGCGCGACGA	CGAGTGTATCC	CGGTCGAGGAC	CTCTCCGCGC	CACCGACGCG	CGCGCGCGTC	6.3
ACCGCGGCTC	CGTCCGAGAC	ATCTTTCGTA	ATCGACGACG	TCCGACGAG	ATATGTCGAC	1.50
CGCGACGCGT	TTCGCTTACG	GACCGACGTC	CGGATCATGT	CGTCGACGCG	TGTCGTCGCG	1.86
CTCACCGACG	TGTACGCTAC	GACCGCGGTC	TCTGTCATCT	CGACGCGCTC	TCTCTGCGAC	2.40
AACCGCGCGG	ACATCTCGTC	TGTCGCGATG	CGCTCGATCG	CGACGCGGCG	CGGATTCGCG	3.60
CTCTCGCGGAC	AATCTGATTT	AGCGACGATG	GGCTTGGCGT	AGGTCGCGCA	TGCTGCCACG	3.60
CTCTGTCGCA	GGCGACGACA	GGTTGCGGCT	GGGTCGCGCT	TGGTCTTTGT	GAGCTGTCGAC	4.20
GGGAGGCTTC	GACCGCGGAC	CGCGACGCTC	CGACGCGACA	ATCGAGGCTC	GTGTC	4.76

(2) INFORMATION FOR SEQ ID NO:128:

1.1 SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1431 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

MOLECULE TYPE: cDNA

14-00000 SOURCE DESCRIPTION: SEQ ID NO: 128

ATGCGCGCGG	GAATAAATA	TTATCGGCAG	GACGGGCGA	ATGCGATGGT	ATATTGCGGT	60
GATGACGCGG	CGGAGAACG	GACTTGTGCG	AGGTCACAG	CTGCTGTAT	TGCTTGCTCG	120
TTAGGCTCTG	GATCGGCGG	GACGGGCAAG	GGGTCGAGG	ACCTCTACG	CGGCGGCTGG	180
TTACAGGATG	GGTTCACGTC	GAGCTGCGCA	CTGTGCGATG	GCGAATGATG	GCGCATCGGG	240
CCACACAGTC	GACGGGCGTC	TAATCGCGGT	GAATGCTGAC	GACGCGGACG	CTCTGGACAG	300
TGGCAACGCG	AGCGGCTCTC	CAATCGGCGG	ACCGAGCGG	TGGGTGGTGT	CGCGGCTGAG	360
CTCTGGAGCG	TGCGGGGTGG	AATCGGCGAT	CTGCTGTGCT	ATGCGGAGAG	CGCGGACGAG	420
GCTCGCTCTG	ACTCGACGCT	CGCGGCGCTG	CGGCGTCCCT	GGGTTCAGAG	GCGCACACGG	480
TTTGGCGCTG	CGAGTGAATG	TGATGTCTTC	CGCGGCTGCT	ACCGGCGCTA	CGACGCGCGC	540
GGTGTGTGTG	CGCAATTGCG	GAGAGCGGAC	TTGAGCAGCG	ATGTCGCGGG	GACGCGCTTG	600
CTCTGGGCGG	GGTGTGCGCG	TGATGTGCGT	GCGGATCGAT	GGTATCTATG	CGCGACGAGG	660
CGCGCGGCGG	CGGAGCGGAA	CGCGCTACAC	GGGCTGCGTC	GCTTTCACCG	GCGGACAGCT	720
TACTTTGCGG	CGGGCATACG	CAGCTCTATG	ACCATATGAG	CGGTGCGGCT	GGGCGGCTGGA	780
CGGCGGCGG	TGCGGACGCG	CGGTGTGTGA	CGGTATGCTG	TGGCGGCGCT	CTATCGACCTG	840

CAGGTCGGCA	CGTTCCAGGT	CTGATGGGTG	CGTTCGATTC	TGCTGGGACT	CGCGTGGCGG	900
GTATCAGCT	GGTAGGTCAG	GAATGTCCTG	AGCAGCTTGG	CGTCAGTCTT	GAGTTGATCT	950
ATAGTGGCG	CGGGCAGCTT	GTGGAATGCG	CGGTTCGTGG	GGCGGAAAC	GGTGTACTCG	1020
CGCGCGTGA	GGGTCGAC	CAGATTACAC	TCCGGGTCA	GCTTCCCGCA	CAGAGCTCGA	1080
GTACGGGTAC	TGAGCATYAG	GTGTGTGAAA	GCCTCGGTCA	CGACGCGCTC	TTGCGGCTAT	1140
CGGGCTCCG	ATCCGGGAC	GGTGCGATTT	TGGCGCGCTT	ATTGGGCGCA	CCACGAGCCA	1200
ATCAGGTTCG	CTGGGTTCAG	CGATGCGCGC	CGTGTGTAAC	GGCGCGCGCG	GGCTGTCTGC	1260
CGGTTCGGG	CTGGTCTTAT	GGACACAGGG	TTTGTGCTG	GAACACCTCG	CTAAGAGCGC	1320
AATCGGATG	GCTCCGAGGC	TGCTGCTGCG	GGCGGCTTTC	GCTTGAATCT	TGATCATCGC	1380
TTGATTCCT	TTGCTTCTGC	GGGGCGGTG	AACCGCTCC	TCTTGGGTGA	A	1440

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) SEQUENCE DESCRIPTION: SEQ ID NO:129:

GCACGAGAGT	CGTATCTTTG	CACCCAGCGC	CGTAGAGAA	CGCTGGGCTT	GGCTAACTGA	60
GATCGGGCG	GCTCTGATTT	CGAGAGGTAA	CGGTCTGCTT	CGCGACAATG	GGTTACCCAC	120
CGAGACTGAT	TGCGCGCGCG	CGGCTTCTGA	CGTGTAGCG	CGGTTCTGTC	CATGCCCCGA	180
ACGGCTGCAC	TACGCGACTT	TCTACGTAGT	AGTGAACGGA	CTTTTACGCA	TATCTCGTGA	240
CGATCTTTGC	CTCCGAGGAC	TCCAGATCTT	ACTCTGCCC			279

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1470 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) SEQUENCE DESCRIPTION: SEQ ID NO:130:

ACCGCCACCC	CGACGCGGGA	ATGACCGTGG	GTAACCTGCC	AAACAAATTT	GTTCCTGAGC	60
GATCTCGGGA	ACAGCGGAATC	CAGGCTGACG	GGCTGATGAG	CTTCTTCTCT	GATGTTCCCA	120
CGGTCGGCGG	CGTGGAGTGA	AACGATACGA	CGGCGCTCT	GGGGGTCAGA	CGCATGAATG	180
TGCTAGCGCG	CGAUCACGCG	CAACGCCGCG	AGAGCTCTGA	TGCGGCTCTG	CAGATTGCGA	240
CGACCAATTA	TGCGCGAGCG	GTGATTTTGG	CGGCAAAAGC	TGAGCGGCGC	ACCTCTGAGC	300
TTCTGCTAGT	GCTCAAGTTC	CTCGGCATAC	AGCGGGGCGA	ACTCAACCGC	GACCGGAGCC	360
GTGCGGAGGA	TGCGGATAGC	GGTGTATGTA	TGCTGATAT	ACACCTTCTG	CAGATCGAGC	420
CCGAAATGCA	TGTGCGCTTG	CGTGGAGCGC	CGGTGACGCG	CGATGAGAAC	ACCGCGCGGG	480
TATTTGAGCG	CGACGATGCT	GGTGGCTTGC	GGCGTGTGCG	CATCGCGCGC	TGCGAGTGGC	540
GTCACCGCGC	TGATCTCTTC	CGGACGCAAC	TCCGCGGCTT	GGCGGCGGCG	GAGATCGAGT	600
GAAAGAGAGT	AGCTCTTACG	CGGCTGTTCG	AGAGAGTGA	TATATGACA	GGCGATCGCG	660
CAACGCGAG	GTGATGTGTC	CGCCTTTTGG	ACGATATGCG	GGAGGAGATC	CTCGGCTTTC	720
TGCTGAGGGA	CGTGTGCGAT	TTGCTGAGAG	AGATGCTGCG	TGCTCTCGGT	CAGCTTTTTC	780
CGACGCTCTT	GGCCCGCGCG	GTTGCTGCGG	GGGATGTGCT	CATCATCGCC	GGCGGCGCGG	840

CCACGGCTTG	TCTGCTCTTG	GGCCATCGCC	GGCTCCGCTC	TGCTCATGCC	CTTTCGAAAG	900
GGCGCGGGTG	CGCTGACAC	GGCTGCTGTC	TTTCTCTCAC	CTACCGGTCA	ACACCGAGCT	960
TTCCCGGCTT	AACCAAGGCT	AGCGAGGCTC	AGCGGTGAGT	TGCTCTACCA	GTCTCCACGGC	1020
ACTGTTCACC	GAATCCAGCA	AGCCACCAAG	ATGCGCTTCA	CTACCCCGCA	ACGGCTCCAG	1080
CGTCGGGATG	GAAACCAAGC	AGTCGGCGCC	AGTGGAGAGA	TCACCGAGTC	CGAGCTAGCG	1140
CGCGCGATAT	CAGCTCCGAA	CGCGCGCAGG	CAATTGCGCC	CGGAAATACG	CGCGGGTGTG	1200
GGTGGCGGCT	TCTCAACGGC	ACTGAGCAGC	TGGTGTTCGG	GTGACTAAAG	GCCTTATGGA	1260
CGCGCGGGCT	ACTAGCGGCT	TGTACAGGCC	CTTGTCCAGC	CGGACATCGG	AGTACTGCGAG	1320
GTTCAGGAGG	TGGCGCCGCG	GGCGCGAGCA	GCTGAGGTTG	TCCCGCTGCC	GGAACCGCTC	1380
GAGCGAGCGC	ACTTTGCGCG	GCTATCTCAG	CAGCTCCGCG	CAATCCATCG	GGTCACGCTC	1440
GAGCTAATCG	AGCACGTGTG	CGCAGGTTTC				1470

(ii) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1059 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) SEQUENCE DESCRIPTION: SEQ ID NO:131:

ATTCCCATCG	CTCGGGCACC	TATCAGTAGG	TAGTGGGTTT	CGATGGTTTT	CGCGGGGCTT	50
TGCGTTGCGC	TGGGCGCAGG	GTCGTTGATG	GGCCCTGCTG	TGCGGATTGG	ATTCTGTGAC	120
AACGAAGATG	GGCGATGGGT	GAGCAATCGT	CGCGGATGCA	AGACACGCTT	TGCGTGGCGC	160
GGCGTCAGGT	GGGCTTAGAG	CGCGGTATAC	AACGTAGACC	GGCCACTGAC	CAAAACCCAA	240
ACCCACAAAC	CTTGACAGCA	TGCGGCTCTC	GGGCTCTCAA	TTCCGGGTAG	ATATCGTATA	300
CGGATATCGG	ATGCGGTAGC	CTTATCGAGG	CATGAGAGCG	CGGCTAGAAC	CACCGGATAT	360
TCCAGATGAG	CTCGGGCGAC	GGCTGGGGCT	CTTGGATGCG	GTGGTGTATG	GGCTTGGGTC	420
CATGATCGGT	CGCGGGAATC	TTGCTCGTGC	CGAATGGGCG	ACGAGCTGCT	GGCGAATTGG	480
GCACGGGATC	CGAATCCCCA	GAGGTTGATG	CAAGCGGTCA	ATGCGCATTG	ATCGTTGGAT	540
CGATGATGAA	CGCTGTGCTC	ATGCGTGGCG	CGTATCTCAA	CGGTCGTCGA	TTGATGCGAT	600
TAGCGTTGGT	TCTGCATTGC	ACCGGTAGGG	CTTACAGTCT	GGCTGTCTATG	CTTGGGCGAT	660
GTCAACAGCT	TTTTTTCAGC	TAGCGAGATC	GTGAGTTTGG	AGTTCGTGAA	GACGGCATGT	720
TGACTTGTGT	TGACTACAT	CGTCTGCGCA	CATTTCGCTT	CGTCAACTG	CGCTGCGACA	780
ATGCGCCAAC	CGCCGTGTAG	CTGCTGCGCA	ATTGGCGAGC	AGGATCCACC	GGAGATGGCC	840
GAGGACTACG	ACHAGGCTTG	GATGCTCAAC	ACCGTGTGCG	ACTATCAGAA	CGAGAACCGCA	900
AAAGAGAGAG	TCATGATCTT	CGTGGCGGAC	GTGAAACRAG	AGAGGGGGGC	CATCGAATCT	960
GTAAAGGAGG	TAGACAAAGA	GGGACATCAG	ACTGCTTACG	GATGGGGGAG	CAGCTTTTCA	1020
TACAGGAGAC	ATCTTAAGTT	TTGATTCGGG	AACATCTTA			1059

(ii) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 153 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) SEQUENCE DESCRIPTION: SEQ ID NO:132:

GCACGAGGCA TTGGCGGGCA TGTGCTATAA CGGTGACGTA TCAGCACAAA ACAGCGGAGA	60
GAACACAGTG CATACAGAAC GTTCCGGGTA GCTGTAGGCC GCAGAGAGTC GTTTCGCTTC	120
GGTGTATTTT CAGACTCTGC AGGACTCGTG GCG	153

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 387 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

CCGCGCGGTC GATCAAGGAG CAGAGCAAAA ACTCCGTCGA GCTCCAGTCG ATGATGCTCA	60
CCCGGCGCAG CATCTGGGCA AGGATCACCT CGATGTGCTT GTCTGGATC GACACAGCTT	120
CGCGCGGCTA GAGCTCTGCG AACTGCCGAA CCAAGTGATP CTGCACTCTG CCGGGGCGCT	180
GCACCGCGAG CAGCTCATGC GGGTGGGCGG AGCTTTCAT CAGCTGCTGG CCGACCTGGA	240
CGTGTCTGCG ATCGGAGAGC AGCGTTTCG AACCTCTTC GTGCTTGAA ACCCGGAGCC	300
GCTGCGCTT GGGAGCTTG TCTTAGACCA CTTCCTCACC GCGCTGTCGA GGAAGATGG	360
TGATTTGTA GAACGCGTGG CCGCTCT	387

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 369 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

GTTCAGCAGC GATATCCGAT TGTGCGGTC GCTTCGGTGG GTCTGAACA CCGCATCGAC	60
ATGCTGCTTC ACAACGAATC CGGACTGCTG GCACGGGTCC AGTTCCTCGC CGAGAGGCTG	120
CTCGGACCCA AAGACGGTCC GCGCGTGGTC CTTGTGTGCG GACTGACACC GTTACCGGCC	180
CCCGAAGGCG AGTATATTAT GTTCGGGAGC CTAACTGACA CCACGAGATT TATGGGCGAG	240
CAACCGAGAG ATAAAGCCGC AAGCAGGGTG CCGGACCGTG CCGCGCGCGC TATCGAGAC	300
GCTATCGAGC TGATGCTGCG CGAGCGGCGA CCGGATCCAA ATGGATCGCT GTCGAGAGCG	360
CTCTAGGCTT CGGAGCGCTA AGGCGGCGC	389

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 480 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

CCCGCGGTCG	GAATGATGCC	CGCTCTGTCG	CGCGCCCTTT	TCATGCTGTT	GAATGAGTGT	60
TTGGAGAGGC	CCGGTTGGCG	TACCGGTGAG	CGGGAATATC	TCATTGGAAGC	GTACCCGGAT	120
GTNCGCATGA	ATNTGNTTGN	CCCGTNGCG	GTNTTGGHTG	GGGAAACACG	GTGTGTGTTA	180
AGCCTTGHTG	GGCTCGAAG	MGCGCTGGAC	GGCTGTGTCG	CCGAGATATA	TSAGCACCTG	240
AGCGTGGTGG	CGATGCCGCT	TATCCCAAGG	AAITGGGAGG	TCGCTCCGCG	AGATGCCGAA	300
GGGTTCGAGG	GTCTGTGTGG	GACTGTCCCG	TCCGHTACCC	CACTCGCGCG	GGGATGTGGG	360
AGCCCGGGG	AGCGTGGCAG	CAGGATCCGG	CGCGCCGCCG	GGAGCAGGCT	CGGNNGTGNN	420
NCGTGHTTC	TNNGGCCGAA	TNNACTGNN	MCNACAACTC	TGNNGCCGAG	TGNNACTGCT	480

(2) INFORMATION FOR SEQ ID NO:136:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 587 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(11) MOLECULE TYPE: cDNA

(12) SEQUENCE DESCRIPTION: SEQ ID NO:136:

GCAGAGGCT	ACCGGGCGGT	CGCGCGCAT	GGCTGTGATG	GAGCGGTAGC	CACCGCTHCA	60
TNCGAGGGT	CAGCGCTGTC	GTCCGGGCTT	AGCGCTATAG	CAGCTGCAAA	GAACCCAGCG	120
CGCGCATTT	CTTTGATGTT	GAACCATGTA	CGCTNCGCTN	CGNUTNCAAT	CTCTCTCTTT	180
NCGCGCGGCG	TATTNNGCC	ATANAATTGG	TNNANNCGN	AGCGGTAGAC	GTATCGAGTT	240
CCCTTTCGAC	CACCGGCTCA	ATTTCAGCA	TCCTATGGGG	ACATGAGCG	CGCGCGCACC	300
GGCGCTTTG	CAATATGTGA	GTTCACACCG	GTCTCAGAG	CGGCGCAAT	GTGCGGCTTA	360
CGGAGCGGCT	GGCTTGCATC	GGTGGGTGA	CGCGCTGCT	TCGCAAGCG	AGGGAAGCTC	420
CGGAGCTCT	ACCGGCCGAA	CGCGCGGGT	GTCACTGATC	TAGGCTGAGC	CGCAGGGGTT	480
GTNAGCGAA	CAAGGATGAG	NACAATAAN	CGGAGGAGAG	ACANNGAAG	GGCGGAGNAG	540
CTNAGCGAG	TTTGNCCAA	MMMACGAC	TNTACGNN	CTTATG		587

(2) INFORMATION FOR SEQ ID NO:137:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1200 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(11) MOLECULE TYPE: cDNA

(12) SEQUENCE DESCRIPTION: SEQ ID NO:137:

CAGGATGAG	CAGAGCGTTC	ATCATCGATC	CAAGGATGAG	TGCTATTGAC	GGCTGTGACG	60
ACCTTTGTGG	GATTGGAATG	CCCAACCAAG	GGGGTATCCY	TTACTTCTCA	CTAGAGTMTG	120
TCGAAAGAGC	CGTGGAGGAG	CTGCGAGGAG	CGTTTCCGCG	TGATGGCTGG	TTAGGTTTGG	180
CGCGGAGGAA	ATAGCGCGCG	AAAGACCGCA	ACGACGTGAA	TTTTTTCAG	GAACCTGKAG	240
ACCTGATATC	TGAGCTATTC	AGCTGTATCC	ACGACCGAGG	CAACCGGGTC	CAGACGACCC	300
GGACATCTCT	GGAGGGCGCC	AGCAAAAGTC	TGCAATTCGT	CGCGCCGGTG	CTGTGTGACC	360
TYACTTACAT	CCCGGTCCTC	GGGACAGCCC	TATCGGCGCG	GTTCAGGCG	CGGTTTTCGG	420
CGGGCGGAGT	GGCGGTAGTG	GGCGCGCGCG	TTCGCTACTT	GGTGTGAA	AGCGTGATCA	480
ACGCGACTCA	ACGCTCTCAA	TTGCTTGCCA	ATTTGGCGGA	GTGCTGCG	CGGCKCATFG	540
CGGACATCAT	TTGCTATGTC	GGGACATCA	TGAAGGCGAC	CCTCGGAGAG	GTGCTGGAGT	600

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TCATACACAA CGCCTCAAC GCCTGAAAG AGCTTTGGGA CAAGTCACG GGGTGGGTGA 660
CCGACTGTTT CTCTCGAGGG TGCTCGAACC TGGAGTCTCTT CTTTCCGGGC GTCTCCGGCT 720
TGACCGGGGC CACCAGCCGC TTCTGGCAG TGACTGGCTT GTTCGGTGGC GCGCTCTCT 780
CCGCTCGCTC GGGCTTGCTT CAGCGGGATA GCCTGGCGAG CTCAGCCAGG TTGGCGCGCC 840
TCCCTGGCAT TGGGGCGGG TCGGCTTTTG GGGGCTTGGC GAGCTTGGCT CAGGTTCATG 900
CCGCTCGAAC TGGCGAGGCG CTAGGGCCCC GAGCTGATGG CCGGTGGGC GCGGTGGCG 960
AGCAGGTCGG CGGGCACTCG CAGCTGCTCT CCGCCAGGGG TTCCCAAGGT ATGGGCGGAC 1020
CGTAGGCTCG GGGCGGCTG CACCTCTCTT CGGGGGCTGC GAAAGGGAGC AGGACCAAGA 1080
AGTACTTGGG AGCGCGGCGG CGCGGCGCTG AGGACGCGGA GCGCGCTCGA CTCGAAGCTG 1140
ACGCGGGCGG TGGCGAAGAG GTGCTGGTAC GAAAGCTCTG CTACGGGCAAT GCGGACCCAA 1200

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(i) INFORMATION FOR SEQ ID NO:138:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 392 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) SEQUENCE DESCRIPTION: SEQ ID NO:138:

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Met Ser Arg Ala Phe Ile Ile Asp Pro Thr Ile Ser Ala Ile Asp Gly
 1           5           10           15
Leu Tyr Asp Leu Leu Gly Ile Gly Ile Pro Asn Gln Gly Gly Ile Leu
20          25          30
Tyr Ser Ser Leu Gln Tyr Phe Gln Lys Ala Leu Gln Gln Leu Ala Ala
35          40          45
Ala Phe Pro Gly Asp Gly Trp Leu Gly Ser Ala Ala Asp Lys Tyr Ala
50          55          60
Gly Lys Asn Arg Asn His Val Asn Phe Phe Gln Gln Leu Ala Asp Leu
65          70          75          80
Asp Arg Gln Leu Ile Ser Leu Ile His Asp Gln Ala Asn Ala Val Gln
85          90          95
Thr Thr Arg Asp Ile Leu Gln Gly Ala Lys Lys Gly Leu Gln Phe Val
100         105         110
Arg Pro Val Ala Val Asp Leu Thr Tyr Ile Pro Val Val Gly His Ala
115         120         125
Leu Ser Ala Ala Phe Gln Ala Pro Phe Cys Ala Gly Ala Met Ala Val
130         135         140
Val Gly Gly Ala Leu Ala Tyr Leu Val Val Lys Thr Leu Ile Asn Ala
145         150         155         160
Thr Gln Leu Leu Lys Leu Leu Ala Lys Leu Ala Gln Leu Val Ala Ala
165         170         175
Ala Ile Ala Asp Ile Ile Ser Asp Val Ala Asp Ile Ile Lys Gly Thr
180         185         190
Leu Gly Gln Val Trp Gln Phe Ile Thr Asn Ala Leu Asn Gly Leu Lys
195         200         205
Gln Leu Trp Asp Lys Leu Thr Gly Trp Val Thr Gly Leu Phe Ser Arg
210         215         220
Gly Trp Ser Asn Leu Gln Ser Phe Phe Ala Gly Val Pro Gly Leu Thr
225         230         235         240
Gly Ala Thr Ser Gly Leu Ser Gln Val Thr Gly Leu Phe Gly Ala Ala
245         250         255

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Gly Leu Ser Ala Ser Ser Gly Leu Ala His Ala Asp Ser Leu Ala Ser
 260 265 270
 Ser Ala Ser Leu Pro Ala Leu Ala Gly Ile Gly Gly Gly Ser Gly Phe
 275 280 285
 Gly Gly Leu Pro Ser Leu Ala Gln Val His Ala Ala Ser Thr Arg Gln
 290 295 300
 Ala Leu Arg Pro Arg Ala Asp Gly Pro Val Gly Ala Ala Ala Gln Gln
 305 310 315 320
 Val Gly Gly Gln Ser Gln Leu Val Ser Ala Gln Gly Ser Gln Gly Met
 325 330 335
 Gly Gly Pro Val Gly Met Gly Gly Met His Pro Ser Ser Gly Ala Ser
 340 345 350
 Lys Gly Thr Thr Thr Lys Lys Tyr Ser Gln Gly Ala Ala Ala Gly Thr
 355 360 365
 Glu Asp Ala Gln Arg Ala Pro Val Glu Ala Asp Ala Gly Gly Gly Gln
 370 375 380
 Lys Val Leu Val Arg Asn Val Val
 385 390

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 435 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

ACGTTTACCC	ATGCCCTCGG	TCCAGAGCAA	CGCCAGACAA	CACAAAGTAA	TATAATTCCG	60
TTATAAAGCA	GACATTTCCG	TGGTATGTGA	GAGATGTGCG	ACCGATCAGA	TTAAGCCGATC	120
CGCGTCAGCT	GATATCGGAT	GTCTTTTGTC	ACCATCCAGC	CGGTGGTCTT	GGCAGCCGGC	180
ACGGAGGACT	TCCGACGAGT	CGGTACCCGC	GTGATGCTTC	GGAAACAGAC	CGTCTGTGCC	240
CGAGGACCG	GGTGTATACC	CGCTGCTGCC	AATGACCTGT	CGTCTCTGAC	GGCGGCTCCG	300
TTACCCGGCC	ACACCAAGCA	CTACCGAGTC	GTGAGTAAGC	CGGAGCGGCT	GGTCCATGGC	360
ATGTTCTGGG	CGCTCCCGGC	GGGCACCGCC	GATGCGTATC	CGACCAACGA	GGCGGCTCAAT	420
GTGTGCGAGA	CGGTTTAA					435

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1441 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

GAGGTTCCTG	GGAATGGATT	TCCGCTTTT	ACCTCCGAA	GGAATTCAA	GGCAATGTA	60
TTCCGCTCCG	GGGCGGAGT	CGATCTAGC	CGCCCGGCC	GCCTGGGAGC	GTGTGGCCGC	120
GAGGTGACT	TCCGCGCGG	TCTCGATGG	ATCGTGTG	TGACGCTGA	TGTTGAGCC	180

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QTGGATGGGG  CCGCGGCGGG  CGCGGATGGC  GCGCGCGGCA  AGCGCGTATG  TGGGGTGGCT  240
GGCGGCGGCG  GCGGCGCGGG  CGAAGGAGAG  GCGGACACAG  GCGAGCGGAG  CGGGCGAGAG  300
GTTTGGGAGG  GCGTTGCGGA  TGAGGGGTGC  AGCATCGCTC  GTGCGGGGCA  ACCGCGAGCG  360
GTTGATGTGG  GTGGTGGCGG  CGAGCATCTC  GCGGCAAAAC  ATTGCGGCGA  TCGCGGCTAC  420
CGAGGCGGAG  TATGCTGAAA  TGTGGGCGCA  AGACGCTGCC  GTGATGTAGC  GCTATGAGGG  480
GGCATGTGCG  GCGCGGTGGG  CGTTGCGGCG  GTTCACTGCA  CGCGTGGAAG  GCACCGGGCC  540
GGCGAGGCGC  CGCGCGCGAG  CGCGCGCGAG  CGAAGCGGCG  GGTGCGGGCG  CGGTTGCGGA  600
TGACAGAGCG  ACACTGGGCG  AGCTGCCGCG  GGGGATGCTG  AGCGACATTC  TGTCGGCGAT  660
GGCGCGGAGC  GGTGATCGCG  TGACAGTGGG  ACTGTTGGGG  ATCGCGGTGA  CGCTCAAGCC  720
CGAGTGGGA  TCGCTCGAG  CGATAGTGAT  CCGTACGCTG  ATAGGGGAT  TGGAGCTGAT  780
CGCGCTCTAC  ATTGCATGCA  TCGGACCGCG  CAGCATTTGG  CTGCGGATCA  CGAACACGGC  840
CAGACCTGGA  CAGATCGGCC  TATCGGGGAA  GCGCGCGGCG  CTGGGACCGA  CGCAGGGGCA  900
TCCATCGAT  TCGGCGAGCG  AGAGAGCGGA  GCGCGACTGG  GGGCGCTTGG  CGGGCGCGCG  960
CGCGGTGCTC  CGGGGGGTGG  GCGACGCGAG  ATTATCTGGA  GCGTTGTGCG  TGCGGCGAGC  1020
CTGGAGGAGC  CGCGCGCGCG  AGATCGAGCT  GCGCGTTGAG  CGAAGAGCGA  CGTTGAGCTC  1080
CAGCGCGGCG  GCGGACCGCG  CGGCGCTTAA  CGGGATTCGG  GCGAGGCTCG  TCGAGGGGAT  1140
GGCTTTGGG  AGCTTGGCGG  CAGCGCGGAG  GAGCGAGGTT  GCGCGGAGCG  GTAGCGGCGC  1200
CAGCACTGAC  GCGGAGAGCG  AGGCGGCGA  AGCGCGGTA  GTTGTGATTA  GAGAGAGGCG  1260
GCGCGCGGGA  AGCGCGCGCG  GGTAAAGTGC  CGGCGAGCGT  TGTGTCGCGG  CGGGAGAAATG  1320
CGTGTGAGC  GTGGCTAGCC  GACGCGCGGT  TCAGACCGCT  TGTATAGTCG  TCGCGGCTATG  1380
GACGAGCGTG  TGTGATTTGT  GCGCGGCTAT  CAGAGCGATT  TTGCTCGGAA  CGTATGAGAA  1440
G

```

(i) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) SEQUENCE DESCRIPTION: SEQ ID NO:141:

```

Met Ser Phe Val Thr Ile Glu Pro Val Val Leu Ala Ala Thr Gly
 1           5           10           15
Asp Leu Pro Thr Ile Gly Thr Ala Val Ser Ala Arg Asn Thr Ala Val
 20           25           30
Cys Ala Pro Thr Thr Gly Val Leu Pro Phe Ala Ala Asn Asp Val Ser
 35           40           45
Val Leu Thr Ala Ala Arg Phe Thr Ala His Thr Lys His Tyr Arg Val
 50           55           60
Val Ser Lys Pro Ala Ala Leu Val His Gly Met Phe Val Ala Leu Pro
 65           70           75           80
Ala Ala Thr Ala Asp Ala Tyr Ala Thr Thr Glu Ala Val Asn Val Val
 85           90           95
Ala Thr Gly

```

(i) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 423 amino acids
- (B) TYPE: amino acid

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(c) STRANDEDNESS: single

(d) TOPOLOGY: linear

(ix) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

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Met Asp Phe Gly Leu Leu Pro Pro Glu Val Asn Ser Ser Arg Met Tyr
 1           5           10           15
Ser Gly Pro Gly Pro Glu Ser Met Leu Ala Ala Ala Ala Trp Asp
 20           25           30
Gly Val Ala Ala Glu Leu Thr Ser Ala Ala Val Ser Tyr Gly Ser Val
 35           40           45
Val Ser Thr Leu Ile Val Glu Pro Trp Met Gly Pro Ala Ala Ala Ala
 50           55           60
Met Ala Ala Ala Ala Thr Pro Tyr Val Gly Trp Leu Ala Ala Thr Ala
 65           70           75           80
Ala Leu Ala Lys Glu Thr Ala Thr Gln Ala Arg Ala Ala Ala Glu Ala
 85           90           95
Phe Gly Thr Ala Phe Ala Met Thr Val Pro Pro Ser Leu Val Ala Ala
100          105          110
Asn Arg Ser Arg Leu Met Ser Leu Val Ala Ala Asn Ile Leu Gly Gln
115          120          125
Asn Ser Ala Ala Ile Ala Ala Thr Gln Ala Glu Tyr Ala Glu Met Trp
130          135          140
Ala Gln Asp Ala Ala Val Met Tyr Ser Tyr Glu Gly Ala Ser Ala Ala
145          150          155
Ala Ser Ala Leu Pro Pro Phe Thr Pro Pro Val Gln Gly Thr Gly Pro
160          165          170          175
Ala Gly Pro Ala Ala Ala Ala Ala Thr Gln Ala Ala Gly Ala Gly
180          185          190
Ala Val Ala Asp Ala Gln Ala Thr Leu Ala Gln Leu Pro Pro Gly Ile
195          200          205
Leu Ser Asp Ile Leu Ser Ala Leu Ala Ala Asn Ala Asp Pro Leu Thr
210          215          220
Ser Gly Leu Leu Gly Ile Ala Ser Thr Leu Asn Pro Gln Val Gly Ser
225          230          235          240
Ala Gln Pro Ile Val Ile Pro Thr Pro Ile Gly Glu Leu Asp Val Ile
245          250          255
Ala Leu Tyr Ile Ala Ser Ile Ala Thr Gly Ser Ile Ala Leu Ala Ile
260          265          270          275
Thr Asn Thr Ala Arg Pro Trp His Ile Gly Leu Tyr Gly Asn Ala Gly
280          285          290
Gly Leu Gly Pro Thr Gln Gly His Pro Leu Ser Ser Ala Thr Asp Glu
295          300          305
Pro Glu Pro His Trp Gly Pro Phe Gly Gly Ala Ala Pro Val Ser Ala
310          315          320
Gly Val Gly His Ala Ala Leu Val Gly Ala Leu Ser Val Pro His Ser
325          330          335
Trp Thr Thr Ala Ala Pro Glu Ile Gln Leu Ala Val Gln Ala Thr Pro
340          345          350          355
Thr Phe Ser Ser Ser Ala Gly Ala Asp Pro Thr Ala Leu Asn Gly Met
360          365          370
Pro Ala Gly Leu Leu Ser Gly Met Ala Leu Ala Ser Leu Ala Ala Arg
375          380          385

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Gly Thr Thr Gly Gly Gly Gly Thr Arg Ser Gly Thr Ser Thr Asp Gly
 385 390 395 400
 Gln Glu Asp Gly Arg Lys Pro Pro Val Val Val Ile Arg Glu Glu Pro
 405 410 415
 Pro Pro Gly Asn Pro Pro Arg
 420

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

Met Ser Leu Leu Asp Ala His Ile Pro Gln Leu Val Ala Ser Gln Ser
 1 5 10 15
 Ala Phe Ala Ala Lys Ala Gly Leu Met Arg His Thr Ile Gly Glu Ala
 20 25 30
 Gln Gln Ala Ala Met Ser Ala Gln Ala Phe His Gln Gly Glu Ser Ser
 35 40 45
 Ala Ala Phe Gln Ala Ala His Ala Arg Phe Val Ala Ala Ala Lys
 50 55 60
 Val Asn Thr Leu Leu Asp Val Ala Gln Ala Asn Leu Gly Glu Ala Ala
 65 70 75 80
 Gly Thr Tyr Val Ala Ala Asp Ala Ala Ala Ser Thr Tyr Thr Gly
 85 90 95
 Phe

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

Cys Arg Leu Cys Leu Asp Ser His Leu Arg Val Val Ala Leu Pro Ala
 1 5 10 15
 Gly Gln Pro Gly Arg Leu Val Gln Ala Ile Gly Pro Ala Gln Glu Arg
 20 25 30
 Asp Val Gly Gln Thr Arg Cys Thr Arg Thr Gly Leu Asp Asa Val Ser
 35 40 45
 Ala Leu Thr Ala Ala Gln Phe Ala Ala His Ala Gln Ile Tyr Gln Ala
 50 55 60
 Val Ser Ala Gln Ala Ala Ala Ile His Glu Met Phe Val Asn Thr Leu

65 70 75 80
Gln Asn Xaa Ser Gly Ser Tyr Ala Ala Thr Glu Ala Ala Asp Ala Ala
 85 90 95
Ala Ala Gly

Claims

1. A polypeptide comprising an antigenic portion of a *M. tuberculosis* antigen, or a variant of said antigen that differs only in conservative substitutions and/or modifications, wherein said antigen comprises an amino acid sequence encoded by a DNA sequence selected from the group consisting of the sequences recited in SEQ ID NO: 1, 11, 12, 83, 103-108, 125, 127, 129-137, 139 and 140, the complements of said sequences, and DNA sequences that hybridize to a sequence recited in SEQ ID NO: 1, 11, 12, 83, 103-108, 125, 127, 129-137, 139 and 140 or a complement thereof under moderately stringent conditions.

2. A polypeptide comprising an immunogenic portion of a *M. tuberculosis* antigen, or a variant of said antigen that differs only in conservative substitutions and/or modifications, wherein said antigen comprises an amino acid sequence selected from the group consisting of sequences recited in SEQ ID NO: 16-33, 109, 126, 138, 141, 142 and variants thereof.

3. A DNA molecule comprising a nucleotide sequence encoding a polypeptide according to any one of claims 1 and 2.

4. A recombinant expression vector comprising a DNA molecule according to claim 3.

5. A host cell transformed with an expression vector according to claim 4.

6. The host cell of claim 5 wherein the host cell is selected from the group consisting of *E. coli*, yeast and mammalian cells.

7. A method for detecting *M. tuberculosis* infection in a biological sample, comprising:

(a) contacting a biological sample with at least one polypeptide according to any one of claims 1 and 2; and

(b) detecting in the sample the presence of antibodies that bind to the polypeptide, thereby detecting *M. tuberculosis* infection in the biological sample.

8. A method for detecting *M. tuberculosis* infection in a biological sample, comprising:

(a) contacting a biological sample with at least one polypeptide encoded by a DNA sequence selected from the group consisting of SEQ ID NO: 2-10, 102, 128, the complements of said sequences, and DNA sequences that hybridize to a sequence recited in SEQ ID NO: 2-10, 102, 128; and

(b) detecting in the sample the presence of antibodies that bind to the polypeptide, thereby detecting *M. tuberculosis* infection in the biological sample.

9. The method of any one of claims 7 and 8 wherein the polypeptide(s) are bound to a solid support.

10. The method of claim 9 wherein the solid support comprises nitrocellulose, latex or a plastic material.

11. The method of any one of claims 7 and 8 wherein the biological sample is selected from the group consisting of whole blood, serum, plasma, saliva, cerebrospinal fluid and urine.

12. The method of claim 11 wherein the biological sample is whole blood or serum.

13. A method for detecting *M. tuberculosis* infection in a biological sample, comprising:

(a) contacting the sample with at least two oligonucleotide primers in a polymerase chain reaction, wherein at least one of the oligonucleotide primers is specific for a DNA molecule according to claim 3; and

(b) detecting in the sample a DNA sequence that amplifies in the presence of the oligonucleotide primers, thereby detecting *M. tuberculosis* infection.

14. The method of claim 13, wherein at least one of the oligonucleotide primers comprises at least about 10 contiguous nucleotides of a DNA molecule according to claim 3.

15. A method for detecting *M. tuberculosis* infection in a biological sample, comprising:

(a) contacting the sample with at least two oligonucleotide primers in a polymerase chain reaction, wherein at least one of the oligonucleotide primers is specific for a DNA sequence selected from the group consisting of SEQ ID NO: 2-10, 102, 128; and

(b) detecting in the sample a DNA sequence that amplifies in the presence of the first and second oligonucleotide primers, thereby detecting *M. tuberculosis* infection.

16. The method of claim 15, wherein at least one of the oligonucleotide primers comprises at least about 10 contiguous nucleotides of a DNA sequence selected from the group consisting of SEQ ID NO: 2-10, 102, 128.

17. The method of claims 13 or 15 wherein the biological sample is selected from the group consisting of whole blood, sputum, serum, plasma, saliva, cerebrospinal fluid and urine.

18. A method for detecting *M. tuberculosis* infection in a biological sample, comprising:

(a) contacting the sample with one or more oligonucleotide probes specific for a DNA molecule according to claim 3; and

(b) detecting in the sample a DNA sequence that hybridizes to the oligonucleotide probe, thereby detecting *M. tuberculosis* infection.

19. The method of claim 18 wherein the probe comprises at least about 15 contiguous nucleotides of a DNA molecule according to claim 3.

20. A method for detecting *M. tuberculosis* infection in a biological sample, comprising:

(a) contacting the sample with one or more oligonucleotide probes specific for a DNA sequence selected from the group consisting of SEQ ID NO: 2-10, 102, 128; and

(b) detecting in the sample a DNA sequence that hybridizes to the oligonucleotide probe, thereby detecting *M. tuberculosis* infection.

21. The method of claim 20 wherein the oligonucleotide probe comprises at least about 15 contiguous nucleotides of a DNA sequence selected from the group consisting of SEQ ID NO: 2-10, 102, 128.

22. The method of claims 18 or 20 wherein the biological sample is selected from the group consisting of whole blood, sputum, serum, plasma, saliva, cerebrospinal fluid and urine.

23. A method for detecting *M. tuberculosis* infection in a biological sample, comprising:

(a) contacting the biological sample with a binding agent which is capable of binding to a polypeptide according to any one of claims 1 and 2; and

(b) detecting in the sample a protein or polypeptide that binds to the binding agent, thereby detecting *M. tuberculosis* infection in the biological sample.

24. A method for detecting *M. tuberculosis* infection in a biological sample, comprising:

(a) contacting the biological sample with a binding agent which is capable of binding to a polypeptide encoded by a DNA sequence selected from the group consisting of SEQ ID NO: 2-10, 102, 128, the complements of said sequences, and DNA sequences that hybridize to a sequence recited in SEQ ID NO: 2-10, 102, 128; and

(b) detecting in the sample a protein or polypeptide that binds to the binding agent, thereby detecting *M. tuberculosis* infection in the biological sample.

25. The method of any one of claims 23 and 24 wherein the binding agent is a monoclonal antibody.

26. The method of any one of claims 23 and 24 wherein the binding agent is a polyclonal antibody.

27. A diagnostic kit comprising:

(a) one or more polypeptides according to any one of claims 1 and 2; and

(b) a detection reagent.

28. A diagnostic kit comprising:

(a) one or more polypeptides encoded by a DNA sequence selected from the group consisting of SEQ ID NO: 2-10, 102, 128, the complements of said sequences, and DNA sequences that hybridize to a sequence recited in SEQ ID NO: 2-10, 102, 128; and

(b) a detection reagent.

29. The kit of any one of claims 27 and 28 wherein the polypeptide(s) are immobilized on a solid support.

30. The kit of any one of claims 27 and 28 wherein the detection reagent comprises a reporter group conjugated to a binding agent.

31. The kit of claim 30 wherein the binding agent is selected from the group consisting of anti-immunoglobulins, Protein G, Protein A and lectins.

32. The kit of claim 30 wherein the reporter group is selected from the group consisting of radioisotopes, fluorescent groups, luminescent groups, enzymes, biotin and dye particles.

33. A diagnostic kit comprising at least two oligonucleotide primers, at least one of the oligonucleotide primers being specific for a DNA molecule according to claim 3.

34. A diagnostic kit according to claim 32, wherein at least one of the oligonucleotide primers comprises at least about 10 contiguous nucleotide of a DNA molecule according to claim 3.

35. A diagnostic kit comprising at least two oligonucleotide primers, at least one of the primers being specific for a DNA sequence selected from the group consisting of SEQ ID NO: 2-10, 102, 128.

36. A diagnostic kit according to claim 35, wherein at least one of the oligonucleotide primers comprises at least about 10 contiguous nucleotide of a DNA sequence selected from the group consisting of SEQ ID NO: 2-10, 102, 128.

37. A diagnostic kit comprising at least one oligonucleotide probe, the oligonucleotide probe being specific for a DNA molecule according to claim 2.

38. A kit according to claim 37, wherein the oligonucleotide probe comprises at least about 15 contiguous nucleotides of a DNA molecule according to claim 3.

39. A diagnostic kit comprising at least one oligonucleotide probe, the oligonucleotide probe being specific for a DNA sequence selected from the group consisting of SEQ ID NO: 2-10, 102, 128.

40. A kit according to claim 39, wherein the oligonucleotide probe comprises at least about 15 contiguous nucleotides of a DNA sequence selected from the group consisting of SEQ ID NO: 2-10, 102, 128.

41. A monoclonal antibody that binds to a polypeptide according to any one of claims 1 and 2.

42. A polyclonal antibody that binds to a polypeptide according to any one of claims 1 and 2.

43. A fusion protein comprising at least two polypeptides according to any one of claims 1 and 2.

44. A fusion protein comprising at least one polypeptide according to claim 1 and a known *M. tuberculosis* antigen.

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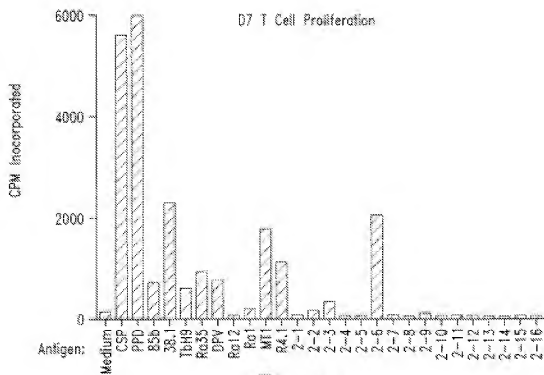


Fig. 1A

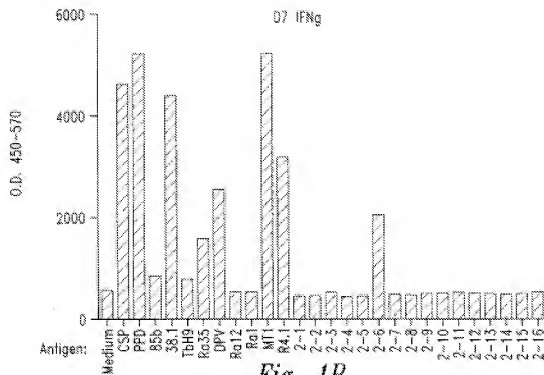


Fig. 1B

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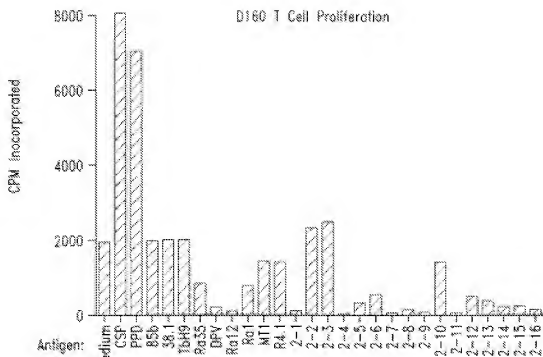


Fig. 2A

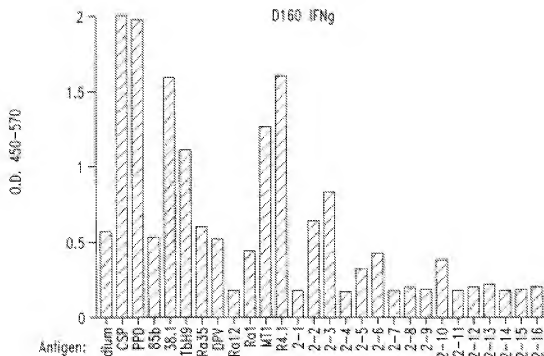


Fig. 2B